
MASSRCH

(TM)

Release 2.1D John F. Collins, Blocomputing Research Unit.
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MPsrch_nnn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jan 8 21:47:01 1998; MasPar time 1479.76 Seconds
Tabular output not generated. 1200.843 Million cell updates/sec

Title: >US-08-943-776-5
Description: (1-1251) from US08943776.seq
Perfect Score: 1251
N.A. Sequence: 1 GTCGACATGAGGACGGCT.....GTGGCCGTGTGGCGCGC 1251
Comp: CAGCTGTACTCTCGTCCGGA.....CACCGGCACATACGCGCGC

Scoring table: TABLE default
Gap 6
Nmatch STD : Dbase 0; Query 0
Searched: 430261 seqs, 710217276 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new7
1: BCT 2: FUN 3: GEN 4: HTG1 5: HTG2 6: HTG3 7: HTG4 8: HDM1
9: HDM2 10: HDM3 11: INV1 12: INV2 13: ORG 14: MAM 15: VRT
16: PLN 17: PRO1 18: PRO2 19: ROD 20: SYN 21: UNC 22: VIR

Database: genbankal01
23: BCT1 24: BCT2 25: BCT3 26: BCT4 27: BCT5 28: BCT6 29: BCT7
30: BCT8 31: BCT9 32: BCT10 33: BCT11 34: BCT12 35: BCT13
36: GEN1 37: GEN2 38: GEN3 39: GEN4 40: GEN5 41: GEN6 42: HTG1
43: HTG2 44: HTG3 45: HTG4 46: HTG5 47: INV1 48: INV2 49: INV3
50: INV4 51: INV5 52: INV6 53: INV7 54: INV8 55: INV9 56: INV10
57: INV11 58: INV12 59: MAM1 60: MAM2 61: MAM3 62: VRT1
63: VRT2 64: VRT3 65: VRT4 66: PAT1 67: PAT2 68: PAT3 69: PAT4
70: PAT5 71: PAT6 72: PAT7 73: PHG 74: PLN1 75: PLN2 76: PLN3
77: PLN4 78: PLN5 79: PLN6 80: PLN7 81: PLN8 82: PLN9 83: PLN10
84: PLN11 85: PLN12 86: PR11 87: PR12 88: PR13 89: PR14
90: PR15 91: PR16 92: PR17 93: PR18 94: PR19 95: PR110
96: PR111 97: PR112 98: PR113 99: PR114 100: PR115 101: PR116
102: PR117 103: ROD1 104: ROD2 105: ROD3 106: ROD4 107: ROD5
108: ROD6 109: ROD7 110: ROD8 111: ROD9 112: STR 113: SYN
114: UNA

Database: genbankb101
115: VRL1 116: VRL2 117: VRL3 118: VRL4 119: VRL5 120: VRL6
121: VRL7 122: VRL8 123: VRL9 124: VRL10 125: VRL11
Database: genbank-new7
126: BCT 127: GEN 128: HTG1 129: HTG2 130: INV 131: MAM
132: VRT 133: PHG 134: PLN1 135: PLN2 136: PR11 137: PR12
138: ROD 139: SYN 140: UNA 141: VRL
Database: u-emb151_101
142: part1 143: part2

Statistics: Mean 11.267; Variance 5.572; scale 2.022
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	406	32.5	1198	96	HSU94504	Human lymphocyte asso	0.00e+00
2	392	31.3	1634	96	HSU74611	Human Apo-3 mRNA, com	1.32e-296
3	390	31.2	1254	96	HSU94501	Human lymphocyte asso	6.74e-295
4	390	31.2	1254	95	HSU72763	Human death receptor	6.74e-295
5	390	31.2	1254	95	HSU78029	Human apoptosis induci	6.74e-295
6	390	31.2	1557	95	HSU73380	Human apoptosis-media	6.74e-295
7	388	31.0	1528	95	HSU83597	Human death domain re	3.44e-293
8	374	29.9	1257	96	HSU94502	Human lymphocyte asso	3.04e-281
9	360	28.8	1119	96	HSU94509	Human lymphocyte asso	2.60e-269
10	341	27.3	1355	96	HSU94503	Human lymphocyte asso	3.87e-253
11	339	27.1	1743	96	HSU94503	H sapiens mRNA for WS	1.94e-251
12	317	25.3	705	96	HSU94508	Human lymphocyte asso	9.38e-233
13	317	25.3	952	96	HSU94506	Human lymphocyte asso	9.38e-233
14	317	25.3	1087	96	HSU94505	Human lymphocyte asso	9.38e-233
15	317	25.3	1143	96	HSU94510	Human lymphocyte asso	9.38e-233
16	300	24.0	838	96	HSU94507	Human lymphocyte asso	2.40e-218
17	177	14.1	808	95	HSU75381	Human apoptosis-media	2.55e-115
18	177	14.1	809	96	HSU94512	Human lymphocyte asso	2.55e-115
19	177	14.1	816	95	HSU83598	Human death domain re	2.55e-115
20	171	13.7	651	95	HSU83599	Human alternatively s	2.24e-110
21	80	6.4	665	95	HSU83600	Human death domain re	1.27e-37
22	53	4.2	281	96	HSU94511	Human lymphocyte asso	8.95e-18
23	40	3.2	215	71	128278	Sequence 5 from paten	5.5e-03
24	37	3.0	1803	54	DROFMRFRN2	Drosophila virilis FM	4.50e-03
25	35	2.8	2431	111	RNU61184	Rattus norvegicus ary	7.82e-04
26	35	2.8	4180	111	RNU49058	Rattus norvegicus CTD	7.82e-04
27	34	2.7	215	71	128278	Sequence 5 from paten	3.38e-03
28	34	2.7	216	98	HUMHUNTPA	Homo sapiens huntingt	3.38e-03
29	34	2.7	614	98	HUMHUN01	Homo sapiens huntingt	3.38e-03
30	34	2.7	3326	52	DMAC000890	Drosophila melanogast	3.38e-03
31	34	2.7	4105	98	HUMHDA	Homo sapiens (clone)	3.38e-03
32	34	2.7	10348	98	HSL191F1	Homo sapiens Huntingt	3.38e-03
33	34	2.7	40592	92	HSL191F1	Equus caballus TATA-b	1.27e-04
34	33	2.6	190	60	HRSTBPRA	H sapiens transcripti	1.27e-04
35	33	2.6	920	93	HSTFIIDAA	Human transcription f	1.27e-04
36	33	2.6	1035	101	HUMFIID	Human TATA-binding pr	1.27e-04
37	33	2.6	1876	101	HUMFIID	Sus scrofa p55 TMR re	1.27e-04
38	33	2.6	2004	61	SSU19994	Rat tumor necrosis fa	1.27e-04
39	33	2.6	2130	110	RATTNFR	Drosophila melanogast	1.27e-04
40	33	2.6	2742	53	DMU82273	Pinctada fucata mRNA	1.27e-04
41	33	2.6	3331	12	PRD074	Drosophila virilis na	1.27e-04
42	33	2.6	5650	54	DROMASTM	Human Notch4 (hNotch4	1.27e-04
43	33	2.6	6122	96	HSU95299	Human Notch4 (hNotch4	1.27e-04
44	33	2.6	19654	9	HSD566	Human DNA for NOTCH4,	1.27e-04
45	33	2.6	19654	86	HSD566	Human DNA for NOTCH4,	1.27e-04

ALIGNMENTS

RESULT 1	HSU94504	1198 bp	mRNA	PRI	15-MAY-1997
LOCUS	Human lymphocyte associated receptor of death 3 mRNA, alternatively spliced, complete cds.				
DEFINITION	U94504				
ACCESSION	U94504				
NID	92071954				
KEYWORDS	human.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
AUTHORS	1 (bases 1 to 1198) Sreaton,G.R., Xu,X.N., Olsen,A.L., Cowper,A.E., Tan,R., McMichael,A.J. and Bell,J.I.				
TITLE	LARD: a new lymphoid-specific death domain containing receptor regulated by alternative pre-mRNA splicing				

[illegible]

D_b 42 gctcctccctggtgctgctgctggtggcccgcccgcccgcccgcccggtgtga 101

[illegible]

QY 66 GCTGCTGCTGCTGCTGCTTTGGTGGCCAGGCGCA-T-GTCGGC-AGGTGGA 122
Db 102 ctgtgcgggtgacttccacaaagatggtctgtttgttgtagaggctgccagcggg 161
QY 123 CTGTGCCAGTAGTCCAGAAAGGATGATGGCCGTTTTTGTACAGGGCTGCCAAGG 182
Db 162 gaactacctgaaggccccttgcaaggagccctgcggcaactcccaactccttgtgttc 221
QY 183 ACATACATGAAGGCCCTCGGCAGAACCCTGTGGCAACTCCACTGCCCTCCCTGTC 242
Db 222 ccaagacacccttcttggtcggtgggagaacacccaataattctgaatgtgccccgtccaggc 281
QY 243 CTCGGACACCTCTGTGACAGAGACAACCATTTTAAGACTGACTGTACCCGCTGCCAAGT 302
Db 282 ctgtgatgagcaggcctcccaagggtggcgctgagaactgttcaagcagtggccagacccg 341
QY 303 CTGTGATGAAGAGGCCCTTCAAGTAGCCCTTGAGAACTGCTCGCAAAGTCGACACCCA 362
Db 342 ctgtggtgttaagcacagctggtttgtggagtgcaggctcagcacaatgtgtcagcagttc 401
QY 363 CTGTGGGTGCCAGTCAGCGCTGTTGACTGCTCCACCGAGCCATGTGGGAAAAGCTC 422
Db 402 acccttctactgccaacatgcttagactgcggggccctgcagccgcacacacagcgctact 461
QY 423 ACCTTCTCTGTGT--C-----CC---A-TGCGGGGC--TACAAC---AC-CA--G-T-C- 462
Db 462 ctgttcccgagagatactgactgtggagctgcctgcctggtcttatgaacaatggoga 521
QY 463 CA--T---G-AG-GCTCAACCCCCCGGCTGCCCTGCTGCTGCTTCTATATACGTGGCAA 515
Db 522 tggctgcgtgtcctgcccacagcaccctgggagctgtccagagcgtgtgcccgt 581
QY 516 TGACTTCAGCTCTGCCCACGGGCTTACAGAGCGTTTGCCCTAAGGCTTGACATGCTGCT 575
Db 582 ctgtggtggagcagatgttctgggtccaggtgtcctctggtggcctgtgggtccct 641
QY 576 CTTGTGGCTGGAGACAGATGTTTGGGTCCAGGTGCT--T--CTAG---GAG-TGCGGTT 626
Db 642 cctgttggggccacctgacctacacacacacccagcactgtggcctcacaagccctgg 701
QY 627 CTTTTTGGGCTATCCTGATCTGTGCATATTGCGATGGCAGCCTTGTAAGGCCGTGGT 686
Db 702 tactgcagatgaagctggatgaggctctgtacccccaccacggccacccatctgtcacc 761
QY 687 CACTGCACACACAGCTGGGACGGAGACCTGGCCTCACACAGACTGCCCATCTCTCAGC 746
Db 762 ctggacagcggccacacccctctagcacctcttcagacagtcagcagtgagaaatctgcacc-- 819
QY 747 CTCAGACAGGCCACACCTCTCTGGCACCTTCCAAAGCAGTACTGGGAAAACTGTACCAC 806
Db 820 -gtccagttgggttaacagctggacccttggctaccgccagacagcagcagcagcagcagc 938
QY 807 TGTCCAGTTGGTAGGCAACAACATGGACCCCTGGCTTATCCCAACTCAGGAGGTGCTGTG 866
Db 879 ccgcaggtgacatggtctgggacagatgtccacagagctcttggccccgtcgtgc 938
QY 867 CGNACAGCCCTCAACACCTGGGATCAGCTGCCAAACAGAACCTTTGGAACCTCTTGCG 926
Db 939 gccacactctccagagatgccccagccggctgcagccaatgactgtagcagccggcc 998
QY 927 ATCTCGCTCTGCGCAGCGCCCTCGGGCTCTCCGGCTGTGTGCTCCAGCCTGGCCC 986
Db 999 gaagctctacgacgtgatggacggtccagcggctgcagccaatgactgtagcagccggcc 1058
QY 987 GCAGCTCTACGATGTATGGATGCGGTGCCAGCAGAGTGAAGAGTTCGTGCGCAC 1046
Db 1059 gctggggctgcgcgaggaagagatcgaagccgtggagtgagatcgccgcttccgaga 1118
QY 1047 GTTGGGCTGCGGGGAAGCGGAAATTGAAGCCGTGGAGTGGAAATCTGCCGCTCCGAGA 1106
Db 1119 ccagcagtcagagatgctcaagcgtgcgcagcagcagcccgccgtcctcgagccgt 1178

QY	1107	CCAGCAGTATGAGATGTCTCAAGCGCTGGCGCTCACGACGACCTGCAGGCCCTCGTGTCAT 1166
Db	1179	ttacgcgcccctgaagcgcattggcggttcgacctgctggaaagacttgcgacgcgcct 1238
QY	1167	CTATCGCGCTCTGGAGCGCATGGGTCTGAAGAGCTGTGCCGAGGACTCTGCCGACGCGCT 1226
Db	1239	gcagcgcggcccgtag 1254
QY	1227	GCAGCGTGGCCCGTAG 1242
RESULT	5	
LOCUS	HSU78029	1254 bp mRNA PRI 16-JAN-1997
DEFINITION	Human apoptosis inducing receptor AIR mRNA, complete cds.	
ACCESSION	U78029	
NID	g1778763	
KEYWORDS	human.	
SOURCE	ORGANISM Homo sapiens	
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;	
REFERENCE	Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AUTHORS	Degli-Esposti,M.A., Din,W.S., Cosman,D., Smith,C.A. and Goodwin,R.G.	
TITLE	AIR, A Novel Member of the TNF Receptor Family, Is a Strong Inducer of Apoptosis	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1254)	
AUTHORS	Degli-Esposti,M.A. and Goodwin,R.G.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-NOV-1996) Biochemistry, Immunex Corporation, 51 University St., Seattle, WA 98101, USA	
FEATURES	Location/Qualifiers	
source	1..1254	
CDS	/organism="Homo sapiens" /chromosome="1" /map="lpter" /cell.type="peripheral blood T-cells" 1..1254 /codon_start=1 /product="apoptosis inducing receptor AIR" /db_xref="PID:g1778764" /translation="NEORPRCAAYAAALLVLGARAGGTRSPRCDADPTLFLFCRCGPAGHYLKAPTEPCNSCLVCPODTFLAWNHNSEACRGCAALALENCASAVADTCGKPGWFEVCQSVSSPFYCQPCLDGALHREIHLICADGCTLPGEYEGEDVCSCPTSLGSCPERRAAGCWRFOWVLVLAGLVWDITTYTRHWHPKPLVTADAEMEALTPPATHLSPLDASHLLAPDSEKELGVNSTPPTYETQALCPQVTSWDLPSRALGPAAPTILSPSPAGSPAMHLEFRLYDVMDVPAREMKFEVTLGLIREAIENAVEIGREFDQQYMLKRWKRCQQAQVTAALERMGDCVEDLSRLQRGP"	
BASE COUNT	201 a 420 c 407 g 226 t	
ORIGIN		
Query Match	31.2%; Score 390; DB 95; Length 1254;	
Best Local Similarity	74.7%; Pred. No. 6,74e-295;	
Matches	908; Conservative 0; Mismatches 266; Indels 42; Gaps 23;	
Db	42	gtctctcttggtgctgctgggggccggccaggcgccactgtagccccaggtgtga 101
QY	66	GCTGTGCTGCTGCTGCTTGGTGCCAGGGCCAGGGCGCA-T-GTCTGGC-AGGTGTGA 122
Db	102	ctgtgcggtgactccacaagaagtgtctgttttgtcagaggtgcccagcggg 161
QY	123	CTGTGCCAGTAGTCCCAGAAGAGGTATGCCCGCTTTTGTTCAGGGGCTGCCAAGGG 182
Db	162	gcactacctgaagggcccttgcacggagccctgcgaactcacctgcttgtygtcc 221
QY	183	ACACTACATGAAGCCCCCTGCGCAGAACCTGTGCAACTCCACCTGCCCTTCCCTGTCC 242
Ddb	222	ccaagacaccttcttggcctgggagaccaccaataatctgaattggccgctgcaggc 281
QY	243	CTCGGACACCTTCTTGACCAGACAACCACTTAAAGCTGACTGTACCCGCTGCCAAGT 302